

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 16:05:26 ; Search time 93 Seconds

(without alignments):
697.902 Million cell updates/sec

Title: US-09-847-809A-3

Perfect score: 1701
Sequence: 1 MDLROFLMCLSLCTAFALSK.....LFGSQATDFGEALVRHDEF 315

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP-ARCHA.21:*
2: SP-Bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organelle:*
9: SP-phage:*
10: SP-plant:*
11: SP-prodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*
15: SP-virus:*
16: SP-bacteriopl:*
17: SP-archaeop:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1583	93.1	315	4	O96RL3
2	1516	89.1	315	11	O35783
3	1491	87.7	296	4	O9NR43
4	1423	83.7	296	6	O9MZ46
5	1031.5	60.6	322	13	O93434
6	905	53.2	322	5	O93136
7	872.5	51.3	328	11	O8R137
8	859.5	50.5	315	11	O99K35
9	842.5	49.5	328	4	O96D15
10	840.5	48.4	328	4	O9BZ8
11	839.5	48.4	329	5	O8SZK6
12	779	45.8	314	5	O23017
13	742.5	43.7	259	11	O9CTD4
14	579	33.0	321	11	O70341
15	564	33.2	192	5	O9W0H8
16	557.5	32.8	193	5	O96051

17	483.5	28.4	342	5	O9VMV2	O9VMV2 drosophila
18	356.5	21.0	313	5	O9TVS8	O9TVS8 caenorhabd
19	297.5	17.5	259	4	O96AA1	O96AA1 homo sapien
20	268.5	15.8	418	5	O9ST97	O9ST97 drosophila
21	257	15.1	391	10	O9FNNO	O9FNNO aradidopsi
22	247	14.5	348	4	O9NZP7	O9NZP7 homo sapien
23	240	14.1	261	5	O9VDY9	O9VDY9 drosophila
24	236	13.9	320	5	O18887	O18887 caenorhabd
25	232.5	13.7	343	5	O9U460	O9U460 plasmodium
26	227.5	13.4	343	5	O25793	O25793 plasmodium
27	222	13.1	98	11	O63399	O63399 rattus nor
28	221.5	13.0	345	10	O9STP7	O9STP7 aradidopsi
29	154	9.1	482	5	O9TZ47	O9TZ47 caenorhabd
30	154	9.1	567	5	O9TZ48	O9TZ48 caenorhabd
31	150.5	8.8	542	5	O9NJD9	O9NJD9 onchocerca
32	146	8.6	165	5	O96609	O96609 dictyostel
33	143	8.4	531	10	O949U0	O949U0 aradidopsi
34	143	8.4	192	10	O9ZSA2	O9ZSA2 aradidopsi
35	143	8.4	1192	5	O96127	O96127 plasmodium
36	142.5	8.4	323	10	O8RWL2	O8RWL2 aradidopsi
37	142.5	8.4	521	10	O9C6P3	O9C6P3 parametium
38	142	8.3	493	5	O15872	O15872 parametium
39	141.5	8.3	553	10	O80700	O80700 aradidopsi
40	141	8.3	465	10	O41793	O41793 zea mays (m
41	140.5	8.3	453	10	O9S9V0	O9S9V0 aradidopsi
42	137	8.1	163	13	O12996	O12996 xenopus lae
43	137	8.1	481	5	O18652	O18652 parametium
44	137	8.1	582	10	O9SI07	O9SI07 aradidopsi
45	136	8.0	540	10	O81390	O81390 nicotiana t

ALIGNMENTS

RESULT 1
ID O96RL3 PRELIMINARY: PRT; 315 AA.
AC O96RL3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Calumenin.
OS Homo, sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Peterson R.E. Jr., Watson D.K.;
RT "Novel splice variant of human calumenin.";
RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF345637; AAK72908.1; -
DR Interpro: IPR02048; EF-hand.
DR Pfam: PF00036; efhand; 6.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_4.
SQ SEQUENCE 315 AA; 37135 MW; EIBF415B25076676 CRC64;

Query Match 93.1%; Score 1583; DB 4; Length 315;
Best Local Similarity 92.7%; Pred. NO. 4.7e-93;
Matches 292; Conservative 10; Mismatches 13; Indels 0; Gaps 0;
OY 1 MDLROFLMCLSLCTAFALSKPTKKRDRVHHPQLSDKVHNDASFDYDHDFAFGAEAKT 60
DB 1 MDLROFLMCLSLCTAFALSKPTKKRDRVHHPQLSDKVHNDASFDYDHDFAFGAEAKT 60
OY 61 FQDLTPESKERLKGIVKIDGKDFVYVDEIKDKIKRAQKWTIEDYEROKKGDVNE 120
DB 61 FQDLTPESKERLKGIVKIDGKDFVYVDEIKDKIKRAQKWTIEDYEROKKGDVNE 120
OY 121 DGVSWEEKKNNATYGVLDPPDPDGFNKKOMVVRDERFRKADKXGDLIATKEEFTAF 180
DB 121 DGVSWEEKKNNATYGVLDPPDPDGFNKKOMVVRDERFRKADKXGDLIATKEEFTAF 180

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DR InterPro: IPR002048; EF-hand.
DR Pfam: PF00036; eFhnd; 6.
DR SMART: SM00054; eFh; 2.
DR PROSITE: PS00018; EF_HAND; 4.
KM Calcium-binding; Endoplasmic reticulum; Signal: Repeat.
FT SIGNAL 1 19
FT CHAIN 20 315 CALUMENIN.
FT CA_BIND 81 92 EF-HAND 1 (POTENTIAL).
FT CA_BIND 117 128 EF-HAND 2 (POTENTIAL).
FT CA_BIND 164 175 EF-HAND 3 (POSSIBLY ANCESTRAL).
FT CA_BIND 201 212 EF-HAND 4 (POTENTIAL).
FT CA_BIND 242 253 EF-HAND 5 (POTENTIAL).
FT CA_BIND 278 289 EF-HAND 6 (POTENTIAL).
FT CAROXYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 312 315 PREVENT SECRETION FROM ER (BY SIMILARITY).
FT CONFLICT 207 207 F -> L (IN REF. 1)
SQ SEQUENCE 315 AA; 37107 MW; 25BAE5A9B527375 CRC64;

Query Match 100.0%; Score 1701; DB 1; Length 315;
Best Local Similarity: 100.0%; Pred. No. 1.8e-94;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLROFLMCLSLCTAFALSKPTKRDVHHEPOLSKVHNDAOSPDYDHAFLGAEEAKT 60
DB 1 MDLROFLMCLSLCTAFALSKPTKRDVHHEPOLSKVHNDAOSPDYDHAFLGAEEAKT 60
QY 61 FQDLPEESKERLGIKIVSKIDGKDFVTVDELKDWIKFAQKRWIYEDVEROMKGDHLE 120
DB 61 FQDLPEESKERLGIKIVSKIDGKDFVTVDELKDWIKFAQKRWIYEDVEROMKGDHLE 120
QY 121 DGLVSWEEYKNNATYGVLDPPDDGFNFKOMVNRDERFRKMAKDGDLIATKEEFTAF 180
DB 121 DGLVSWEEYKNNATYGVLDPPDDGFNFKOMVNRDERFRKMAKDGDLIATKEEFTAF 180
QY 181 HPEEYVYMDIYVQETMEDIDKNADGFIDLEEYIGMYSHDGTDEPENVKTEREQFVE 240
DB 181 HPEEYVYMDIYVQETMEDIDKNADGFIDLEEYIGMYSHDGTDEPENVKTEREQFVE 240
QY 241 RDKNRDGMKDKETKDWILIPSDYDHAEAERHLYVESDONKDKGLTKEEIVDKYDLFVGS 300
DB 241 RDKNRDGMKDKETKDWILIPSDYDHAEAERHLYVESDONKDKGLTKEEIVDKYDLFVGS 300
QY 301 QATDFGEALVRHDEF 315
DB 301 QATDFGEALVRHDEF 315

RESULT 2
CALU_MOUSE STANDARD; PRT; 315 AA.
AC 035887;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Calumenin precursor.
GN CALU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=ICR; TISSUE=Heart;
MEDLINE=97364750; PubMed=9218460;
RA Yabe D., Nakamura T., Kanazawa N., Tashiro K., Honjo T.;
RT Calumenin, a Ca2+-binding protein retained in the endoplasmic
reticulum with a novel carboxyl-terminal sequence, HDEF-";
RL J. Biol. Chem. 272:18232-18239(1997).
CC -1- FUNCTION: NOT KNOWN, BINDS 7 CALCIUM IONS WITH A LOW AFFINITY (BY
similarity).
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CREC FAMILY.

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CC -1- SIMILARITY: CONTAINS 6 EF-HAND CALCIUM-BINDING DOMAINS.
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CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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DR EMBL: U81829; AAC53316.1; -.
DR MGI: MGI:1097158; Calu.
DR InterPro: IPR002048; EF-hand.
DR Pfam: PF00036; eFhnd; 6.
DR SMART: SM00054; eFh; 2.
DR PROSITE: PS00018; EF_HAND; 4.
KM Calcium-binding; Endoplasmic reticulum; Signal: Repeat.
FT SIGNAL 1 19
FT CHAIN 20 315 CALUMENIN.
FT CA_BIND 81 92 EF-HAND 1 (POTENTIAL).
FT CA_BIND 117 128 EF-HAND 2 (POTENTIAL).
FT CA_BIND 164 175 EF-HAND 3 (POSSIBLY ANCESTRAL).
FT CA_BIND 201 212 EF-HAND 4 (POTENTIAL).
FT CA_BIND 242 253 EF-HAND 5 (POTENTIAL).
FT CA_BIND 278 289 EF-HAND 6 (POTENTIAL).
FT CAROXYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 312 315 PREVENT SECRETION FROM ER.
SQ SEQUENCE 315 AA; 37063 MW; 742361814171E273 CRC64;

Query Match 98.2%; Score 1670; DB 1; Length 315;
Best Local Similarity: 98.1%; Pred. No. 1.2e-92;
Matches 309; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDLROFLMCLSLCTAFALSKPTKRDVHHEPOLSKVHNDAOSPDYDHAFLGAEEAKT 60
DB 1 MDLROFLMCLSLCTAFALSKPTKRDVHHEPOLSKVHNDAOSPDYDHAFLGAEEAKS 60
QY 61 FQDLPEESKERLGIKIVSKIDGKDFVTVDELKDWIKFAQKRWIYEDVEROMKGDHLE 120
DB 61 FQDLPEESKERLGIKIVSKIDGKDFVTVDELKDWIKFAQKRWIYEDVEROMKGDHLE 120
QY 121 DGLVSWEEYKNNATYGVLDPPDDGFNFKOMVNRDERFRKMAKDGDLIATKEEFTAF 180
DB 121 DGLVSWEEYKNNATYGVLDPPDDGFNFKOMVNRDERFRKMAKDGDLIATKEEFTAF 180
QY 181 HPEEYVYMDIYVQETMEDIDKNADGFIDLEEYIGMYSHDGTDEPENVKTEREQFVE 240
DB 181 HPEEYVYMDIYVQETMEDIDKNADGFIDLEEYIGMYSHDGTDEPENVKTEREQFVE 240
QY 241 RDKNRDGMKDKETKDWILIPSDYDHAEAERHLYVESDONKDKGLTKEEIVDKYDLFVGS 300
DB 241 RDKNRDGMKDKETKDWILIPSDYDHAEAERHLYVESDONKDKGLTKEEIVDKYDLFVGS 300
QY 301 QATDFGEALVRHDEF 315
DB 301 QATDFGEALVRHDEF 315

RESULT 3
RCN1_HUMAN STANDARD; PRT; 331 AA.
AC Q15293;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Reticulocalbin 1 precursor.
GN RCN1 OR RCN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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QY 181 HPEEYVMDIVVOETMEDIDKNADGFIIDLEEYIGDMYSHDGNDEPEMYKTEREQVEE 240
 DB 181 HPEEYVMDIVVOETMEDIDKNADGFIIDLEEYIGDMYSHDGNDEPEMYKTEREQVEE 240
 QY 241 RDNKRDGKMDKEETKDWILPSDYDHAFAEARNHYVESDQNKDGKLTKEEIVDKYDLFVGS 300
 DB 241 RDNKRDGKMDKEETKDWILPSDYDHAFAEARNHYVESDQNKDGKLTKEEIVDKYDLFVGS 300
 QY 301 QATDFGEALVRHDEF 315
 DB 301 QATDFGEALVRHDEF 315

RESULT 2

035783 PRELIMINARY; PRT; 315 AA.
 ID 035783;
 AC 035783;
 DT 01-JAN-1998 (TReMBLrel. 05, Created)
 DT 01-JUN-1998 (TReMBLrel. 05, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE CBP-50 protein.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NC NCB1_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
 RA Hsueh M.J.;
 RL Submitted (OCT-1997) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
 RX MEDLINE=93107083; PubMed=9416973;
 RA Ozawa, M., Muramatsu, T.;
 RT "Retinoid-inducible: a novel endoplasmic reticulum resident calcium-binding protein with multiple EF-hand motifs and a coxoyl-terminal HDRL sequence."
 RL J. Biol. Chem. 268:699-705(1993).
 DR EMBL: AJ001929; CAA05100.1;
 DR InterPro: IPR02048; EF-hand.
 DR Pfam: PF00036; ehand; 6.
 DR SMART: SM00054; Efh; 2.
 DR PROSITE: PS00018; EF_HAND; UNKNOWN_4.
 SQ SEQUENCE 315 AA; 3696 MW; 06B/FED57929B98 CRC64;

Query Match 89.1%; Score 1516; DB 11; Length 315;
 Best Local Similarity 88.6%; Pred. No. 8.3e-89;
 Matches 279; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

QY 1 MDLRQFLMCLSLCTAFALSKPTKRDVHHEPOLSDKYHNDQSFYDHDHAFLEGADEAKT 60
 DB 1 MDLRQFLMCLSLCTAFALSKPTKRDVHHEPOLSDKYHNDQSFYDHDHAFLEGADEAKS 60
 QY 61 FDQLTPRESKRELKGIYVKGIDGKGFVYDELKDKMIFKFAOKRWIYEDVEROMKGDHLE 120
 DB 61 FGQLTPRESKRELKGIYVKGIDGKGFVYDELKDKMIFKFAOKRWIYEDVEROMKGDHLE 120
 QY 61 FGQLTPRESKRELKGIYVKGIDGKGFVYDELKDKMIFKFAOKRWIYEDVEROMKGDHLE 120
 DB 61 FGQLTPRESKRELKGIYVKGIDGKGFVYDELKDKMIFKFAOKRWIYEDVEROMKGDHLE 120
 QY 121 DGLVMEEEKKNATYGYVLDPPDDGFNYKQAMVDERFRKADKDGDLIATKEEFTAF 180
 DB 121 DGLVMEEEKKNATYGYVLDPPDDGFNYKQAMVDERFRKADKDGDLIATKEEFTAF 180
 QY 181 HPEEYVMDIVVOETMEDIDKNADGFIIDLEEYIGDMYSHDGNDEPEMYKTEREQVEE 240
 DB 181 HPEEYVMDIVVOETMEDIDKNADGFIIDLEEYIGDMYSHDGNDEPEMYKTEREQVEE 240
 QY 241 RDNKRDGKMDKEETKDWILPSDYDHAFAEARNHYVESDQNKDGKLTKEEIVDKYDLFVGS 300
 DB 241 RDNKRDGKMDKEETKDWILPSDYDHAFAEARNHYVESDQNKDGKLTKEEIVDKYDLFVGS 300
 QY 301 QATDFGEALVRHDEF 315
 DB 301 QATDFGEALVRHDEF 315

RESULT 3

09NR43 PRELIMINARY; PRT; 296 AA.
 ID 09NR43;
 AC 09NR43;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Crocalbin-like protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NC NCB1_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RX MEDLINE=99192326; PubMed=10094503;
 RA Hsueh M.J., Yen C.H., Tzeng M.C.;
 RT "Crocalbin: a new calcium-binding protein that is also a binding protein for crotoxin, a neurotoxic phospholipase A2."
 RL FEBS Lett. 445:440-444(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RA Hsueh M.J., Tzeng M.C.;
 RL Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF257659; AAF76141.1;
 DR InterPro: IPR02048; EF-hand.
 DR Pfam: PF00036; ehand; 6.
 DR SMART: SM00054; Efh; 3.
 DR PROSITE: PS00018; EF_HAND; UNKNOWN_4.
 FT NON-TER
 SQ SEQUENCE 296 AA; 34990 MW; D011D029ADEA02E CRC64;

Query Match 87.7%; Score 1491; DB 4; Length 296;
 Best Local Similarity 92.6%; Pred. No. 3e-87;
 Matches 274; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 20 KPTKKRDVHHEPOLSDKYHNDQSFYDHDHAFLEGADEAKTDDQLTPRESKRELKGIYK 79
 DB 1 KPTKKRDVHHEPOLSDKYHNDQSFYDHDHAFLEGADEAKTDDQLTPRESKRELKGIYDK 60
 QY 80 IDGDKGFVYDELKDKMIFKFAOKRWIYEDVEROMKGDHLENDGLVSWEEKKNATYGYLD 139
 DB 61 IDADKGFVYDELKDKMIFKFAOKRWIYEDVEROMKGDHLENDGLVSWEEKKNATYGYLD 120
 QY 140 DDDPDDGFNYKQAMVDERFRKADKDGDLIATKEEFTAFLEHPEEYDKKDIYVOETMED 199
 DB 121 DDDPDDGFNYKQAMVDERFRKADKDGDLIATKEEFTAFLEHPEEYDKKDIYVOETMED 180
 QY 200 IDKNADGFIIDLEEYIGDMYSHDGNDEPEMYKTEREQVEEFDKNDGMDKEETKDWIL 259
 DB 181 IDKNADGFIIDLEEYIGDMYSHDGNDEPEMYKTEREQVEEFDKNDGMDKEETKDWIL 240
 QY 260 PSDDYDHAFAEARNHYVESDQNKDGKLTKEEIVDKYDLFVGSQATDFGEALVRHDEF 315
 DB 241 PSDDYDHAFAEARNHYVESDQNKDGKLTKEEIVDKYDLFVGSQATDFGEALVRHDEF 296
 RESULT 4
 09MZ46 PRELIMINARY; PRT; 296 AA.
 ID 09MZ46;
 AC 09MZ46;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE Crocalbin-like protein (Fragment).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 NC NCB1_Taxid=9823;
 RN [1]